



Application No. 10/808,187

Docket No.: V9661.0078

AMENDMENTS TO THE CLAIMS

1. (Previously Presented) An isolated nucleic acid molecule consisting essentially of the nucleic acid sequence of SEQ ID NO:2471, 2472, or a complement thereof, wherein said nucleic acid molecule is 100 nucleotides or less in length.

2. (Previously Presented) An isolated nucleic acid molecule consisting essentially of the nucleic acid sequence of SEQ ID NO:2474, 2475, or a complement thereof, wherein said nucleic acid molecule is 100 nucleotides or less in length.

3. (Previously Presented) An isolated nucleic acid molecule consisting essentially of the nucleic acid sequence of SEQ ID NO:2473, or a complement thereof, wherein said nucleic acid molecule is 100 nucleotides or less in length.

4-10. (Cancelled).

11. (Previously Presented) A method for detecting the presence of the hSARS virus in a biological sample, said method comprising:

(a) amplifying a nucleic acid from said sample using primers, one of which consists of the nucleic acid sequence of SEQ ID NOS:2471 or 2472;

(b) detecting in the nucleic acid using a probe consisting of the nucleic acid sequence of SEQ ID NO:2473; and

(c) wherein said detecting indicates the presence of the hSARS virus in said sample.

12. (Previously Presented) A method for detecting the presence of the hSARS virus in a biological sample, said method comprising:

(a) amplifying a nucleic acid from said sample using primers, one of which consists of the nucleic acid sequence of SEQ ID NOS:2474 or 2475;

- (b) detecting in the nucleic acid using a probe consisting of the nucleic acid sequence of SEQ ID NO:2476; and
- (c) wherein said detecting indicates the presence of the hSARS virus in said sample.

13. (Cancelled).

14. (Previously Presented) A method for identifying a subject infected with the hSARS virus, said method comprising:

- (a) obtaining total RNA from a biological sample obtained from the subject
- (b) reverse transcribing the total RNA to obtain cDNA;
- (c) subjecting the cDNA to PCR assay using a set of primers, one of which consists of the nucleic acid sequence of SEQ ID NOS:2471 or 2472;
- (d) detecting a product of PCR assay; and
- (e) wherein said detecting indicates that the subject is infected with hSARS virus.

15. (Previously Presented) The method of claim 14, wherein said product in step (d) is detected with a probe.

16. (Previously Presented) The method of claim 15, wherein the probe is a nucleic acid molecule consisting of the nucleotide sequence of SEQ ID NO:2473.

17. (Previously Presented) A method for identifying a subject infected with the hSARS virus, said method comprising:

- (a) obtaining total RNA from a biological sample obtained from the subject
- (b) reverse transcribing the total RNA to obtain cDNA;

(c) subjecting the cDNA to PCR assay using a set of primers, one of which consists of the nucleic acid sequence of SEQ ID NOS:2474 or 2475;

(d) detecting a product of PCR assay; and

(e) wherein said detecting indicates that the subject is infected with hSARS virus.

18. (Previously Presented) The method of claim 17, wherein said product in step (d) is detected with a probe.

19. (Previously Presented) The method of claim 18, wherein the probe is a nucleic acid molecule consisting of the nucleotide sequence of SEQ ID NO:2476.

20. (Previously Presented) A kit comprising in one or more containers one or more isolated nucleic acid molecules consisting essentially of a nucleotide sequence selected from the group consisting of SEQ ID NO:2471, SEQ ID NO:2472, and SEQ ID NO:2473, wherein the nucleic acid molecule or molecules are 100 nucleotides or less in length.

21. (Previously Presented) A kit comprising in one or more containers a polymerase and one or more isolated nucleic acid molecules consisting essentially of a nucleotide sequence selected from the group consisting of SEQ ID NO:2474, SEQ ID NO:2475, and SEQ ID NO:2476, wherein the nucleic acid molecule or molecules are 100 nucleotides or less in length.

22. (Previously Presented) An isolated nucleic acid molecule consisting essentially of at least 15 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:2471, 2472, or a complement thereof, wherein said nucleic acid molecule is 100 nucleotides or less in length.

23. (Previously Presented) An isolated nucleic acid molecule consisting essentially of at least 15 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:2474, 2475, or a complement thereof, wherein said nucleic acid molecule is 100 nucleotides or less in length.

24 (Previously Presented) An isolated nucleic acid molecule consisting essentially of at least 15 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:2473, or a complement thereof, wherein said nucleic acid molecule is 100 nucleotides or less in length.

25. (Previously Presented) A method for identifying a subject infected with the hSARS virus, said method comprising:

- (a) obtaining total RNA from a biological sample obtained from the subject
- (b) reverse transcribing the total RNA to obtain cDNA; and
- (c) subjecting the cDNA to PCR assay using a set of primers, one of which is a nucleic acid molecule consisting essentially of at least 10 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:2471, 2472, or a complement thereof;
- (d) detecting a product of PCR assay; and
- (e) wherein said detecting indicates that the subject is infected with hSARS virus.

26. (Previously Presented) The method of claim 25, wherein said product in step (d) is detected with a probe.

27. (Previously Presented) The method of claim 26, wherein the probe is a nucleic acid molecule consisting essentially of at least 10 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:2473.

28. (Previously Presented) A method for identifying a subject infected with the hSARS virus, said method comprising:

- (a) obtaining total RNA from a biological sample obtained from the subject
- (b) reverse transcribing the total RNA to obtain cDNA; and
- (c) subjecting the cDNA to PCR assay using a set of primers, one of which is a nucleic acid molecule consisting essentially of at least 10 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:2474, 2475, or a complement thereof;
- (d) detecting a product of PCR assay; and
- (e) wherein said detecting indicates that the subject is infected with hSARS virus.

29. (Previously Presented) The method of claim 28 wherein said product in step (d) is detected with a probe.

30. (Previously Presented) The method of claim 29, wherein the probe is a nucleic acid molecule consisting essentially of at least 10 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:2476.

31. (Previously Presented) An isolated nucleic acid molecule consisting essentially of at least 15 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:2476, or a complement thereof, wherein said nucleic acid molecule is from 25 to 100 nucleotides inclusive in length.

32. (Previously Presented) A kit comprising in one or more containers one or more isolated nucleic acid molecules consisting essentially of a nucleotide sequence selected from the group consisting of SEQ ID NO:2474 and SEQ ID NO:2475, wherein the nucleic acid molecule or molecules are 100 nucleotides or less in length.